



Does Not Comply
Corrected Diskette Needed

1600

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/788,308A

DATE: 04/16/2002
TIME: 14:41:16

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Input Set : F:\Northwestern-6374-US.ST25.txt
Output Set: N:\CRF3\04162002\I788308A.raw

3 <110> APPLICANT: Northwestern University
5 <120> TITLE OF INVENTION: Polypeptoid Pulmonary Surfactants
7 <130> FILE REFERENCE: 6374
9 <140> CURRENT APPLICATION NUMBER: US 09/788,308A
10 <141> CURRENT FILING DATE: 2001-02-16
12 <150> PRIOR APPLICATION NUMBER: US 60/182,847
13 <151> PRIOR FILING DATE: 2000-02-16
15 <160> NUMBER OF SEQ ID NOS: 4
17 <170> SOFTWARE: PatentIn version 3.1
19 <210> SEQ ID NO: 1
20 <211> LENGTH: 9
21 <212> TYPE: PRT
22 <213> ORGANISM: Homo sapiens
24 <220> FEATURE:
25 <221> NAME/KEY: MISC_FEATURE
26 <222> LOCATION: (1)..(2)
27 <223> OTHER INFORMATION: Either Phe, Cys with an attached palmitoyl residue, or N-substitu
28 ted peptoid
31 <220> FEATURE:
32 <221> NAME/KEY: MISC_FEATURE
33 <222> LOCATION: (9)..(9)
34 <223> OTHER INFORMATION: 13-20 N-substituted peptoids
37 <400> SEQUENCE: 1
W--> 39 Xaa Xaa Pro Val His Leu Lys Arg Xaa
40 1 5
43 <210> SEQ ID NO: 2
44 <211> LENGTH: 79
45 <212> TYPE: PRT
46 <213> ORGANISM: Homo sapiens
48 <400> SEQUENCE: 2
50 Phe Pro Ile Pro Leu Pro Tyr Cys Trp Leu Cys Arg Ala Leu Ile Lys
51 1 5 10 15
54 Arg Ile Gln Ala Met Ile Pro Lys Gly Ala Leu Arg Val Ala Val Ala
55 20 25 30
58 Gln Val Cys Arg Val Val Pro Leu Val Ala Gly Gly Ile Cys Gln Cys
59 35 40 45
62 Leu Ala Glu Arg Tyr Ser Val Ile Leu Leu Asp Thr Leu Leu Gly Arg
63 50 55 60
66 Met Leu Pro Gln Leu Val Cys Arg Leu Val Leu Arg Cys Ser Met
67 65 70 75
70 <210> SEQ ID NO: 3
71 <211> LENGTH: 35
72 <212> TYPE: PRT

Xaa commonly represent a single amino acid.
See error summary sheet

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73 <213> ORGANISM: Homo sapiens

75 <400> SEQUENCE: 3

77 Phe Gly Ile Pro Cys Cys Pro Val His Leu Lys Arg Leu Leu Ile Val

78 1 5 10 15

81 Val Val Val Val Val Leu Ile Val Val Val Ile Val Gly Ala Leu Leu

82 20 25 30

85 Met Gly Leu

86 35

89 <210> SEQ ID NO: 4

90 <211> LENGTH: 9

91 <212> TYPE: PRT

92 <213> ORGANISM: Homo sapiens

94 <220> FEATURE:

95 <221> NAME/KEY: MISC_FEATURE

96 <222> LOCATION: (9)..(9)

97 <223> OTHER INFORMATION: (15 N-substituted peptoids) → See vme e rict

100 <400> SEQUENCE: 4

W--> 102 Phe Phe Pro Val His Leu Lys Arg Xaa

103 1 5

RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/09/788,308A

DATE: 04/16/2002
TIME: 14:41:17

Input Set : F:\Northwestern-6374-US.ST25.txt
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:1; Xaa Pos. 1,2,9

Seq#:4; Xaa Pos. 9

VERIFICATION SUMMARY

DATE: 04/16/2002

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Input Set : F:\Northwestern-6374-US.ST25.txt

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L:39 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:0

L:102 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4 after pos.:0

Raw Sequence Listing Error Summary

1600

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER: 09/788,308A

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 ☐ Wrapped Nucleics
Wrapped Aminos
The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 ☐ Invalid Line Length
The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 ☐ Misaligned Amino
Numbering
The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 ☐ Non-ASCII
The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 ☒ Variable Length
Sequence(s) 14 contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 ☐ PatentIn 2.0
"bug"
A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s). Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 ☐ Skipped Sequences
(OLD RULES)
Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 ☐ Skipped Sequences
(NEW RULES)
Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000
- 9 ☐ Use of n's or Xaa's
(NEW RULES)
Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10 ☐ Invalid <213>
Response
Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11 ☐ Use of <220>
Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses.
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 ☐ PatentIn 2.0
"bug"
Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 ☐ Misuse of n
n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

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